



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/718,000

DATE: 08/27/2004

TIME: 11:39:15

Input Set : N:\Crf3\RULE60\10718000.raw

Output Set: N:\CRF4\08272004\J718000.raw

1 <110> APPLICANT: KRINGELUM, Boerge  
 2 Nilsson, Dan  
 3 SOERENSEN, Kim I.  
 4 <120> TITLE OF INVENTION: METHOD OF IMPROVING THE EFFICACY OF LACTIC ACID BACTERIAL

STARTER

5 CULTURES AND IMPROVED STARTER CULTURE COMPOSITIONS  
 6 <130> FILE REFERENCE: KRINGELUM=1A  
 7 <140> CURRENT APPLICATION NUMBER: US/10/718,000  
 8 <141> CURRENT FILING DATE: 2003-11-21  
 9 <150> PRIOR APPLICATION NUMBER: US/09/879,036  
 10 <151> PRIOR FILING DATE: 2001-06-13  
 11 <150> PRIOR APPLICATION NUMBER: US 09/086,722  
 12 <151> PRIOR FILING DATE: 1998-05-29  
 13 <150> PRIOR APPLICATION NUMBER: PCT/DK98/00210  
 14 <151> PRIOR FILING DATE: 1998-05-25  
 15 <150> PRIOR APPLICATION NUMBER: US 60/048,337  
 16 <151> PRIOR FILING DATE: 1997-05-30  
 17 <150> PRIOR APPLICATION NUMBER: DK 0633/97  
 18 <151> PRIOR FILING DATE: 1997-05-30  
 19 <160> NUMBER OF SEQ ID NOS: 2  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1638  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Lactococcus lactis  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (255)..(1580)  
 29 <223> OTHER INFORMATION:

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32	gcttttgcatt cagaaactat gtggcaagct taataataaa tctgtcaaaa taattttattt	120
33	tgcacatgtt ttatctaa taattaaaaat aattatttca caatgttcac aagcgcttac	180
34	aaaagaaaaat agattgactt atgctaaact gaataatgta aaaagaattt tacatttaaa	240
35	ggagacctat tagt atg aaa atc gta gtt atc ggt aca aac cac gca ggc	290
36	Met Lys Ile Val Val Ile Gly Thr Asn His Ala Gly	
37	1 5 10	
38	att gct aca gcg aat aca tta ctt gaa caa tat ccc ggg cat gaa att	338
39	Ile Ala Thr Ala Asn Thr Leu Leu Glu Gln Tyr Pro Gly His Glu Ile	
40	15 20 25	
41	gtc atg att gac cgt aat agc aac atg agt tat cta ggt tgt ggc aca	386
42	Val Met Ile Asp Arg Asn Ser Asn Met Ser Tyr Leu Gly Cys Gly Thr	
43	30 35 40	
44	gca att tgg gtt gga aga caa att gaa aaa cca gat gaa tta ttt tat	434

ENTERED

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45	Ala Ile Trp Val Gly Arg Gln Ile Glu Lys Pro Asp Glu Leu Phe Tyr		
46	45 50 55 60		
47	gcc aaa gca gag gat ttt gag gca aaa ggg gta aaa att ttg act gaa	482	
48	Ala Lys Ala Glu Asp Phe Glu Ala Lys Gly Val Lys Ile Leu Thr Glu		
49	65 70 75		
50	aca gaa gtt tca gaa att gat ttt gct aat aag aaa gtt tat gca aaa	530	
51	Thr Glu Val Ser Glu Ile Asp Phe Ala Asn Lys Lys Val Tyr Ala Lys		
52	80 85 90		
53	act aaa tct gat gat gaa ata att gaa gct tac gac aag ctt gtt tta	578	
54	Thr Lys Ser Asp Asp Glu Ile Ile Glu Ala Tyr Asp Lys Leu Val Leu		
55	95 100 105		
56	gca aca ggt tca cgt cca att att cct aat cta cca ggc aaa gac ctt	626	
57	Ala Thr Gly Ser Arg Pro Ile Ile Pro Asn Leu Pro Gly Lys Asp Leu		
58	110 115 120		
59	aag gga att cat ttt ctg aaa ctt ttt caa gaa ggt caa gca att gac	674	
60	Lys Gly Ile His Phe Leu Lys Leu Phe Gln Glu Gly Gln Ala Ile Asp		
61	125 130 135 140		
62	gca gaa ttt gcc aaa gaa aaa gtc aag cgt atc gca gtc att ggt gca	722	
63	Ala Glu Phe Ala Lys Glu Lys Val Lys Arg Ile Ala Val Ile Gly Ala		
64	145 150 155		
65	gga tat atc ggt aca gag att gcg gaa gca gct aaa cgt cgg ggt aaa	770	
66	Gly Tyr Ile Gly Thr Glu Ile Ala Glu Ala Ala Lys Arg Arg Gly Lys		
67	160 165 170		
68	gaa gtt ctt ctc ttt gac gct gaa aat act tca ctt gca tca tat tat	818	
69	Glu Val Leu Leu Phe Asp Ala Glu Asn Thr Ser Leu Ala Ser Tyr Tyr		
70	175 180 185		
71	gat gaa gaa ttt gcc aaa gga atg gat gaa aac ctt gct caa cat gga	866	
72	Asp Glu Glu Phe Ala Lys Gly Met Asp Glu Asn Leu Ala Gln His Gly		
73	190 195 200		
74	att gaa ctt cat ttt gga caa ctg gcc aaa gaa ttt aaa gcg aat gag	914	
75	Ile Glu Leu His Phe Gly Gln Leu Ala Lys Glu Phe Lys Ala Asn Glu		
76	205 210 215 220		
77	gaa ggt tat gta tca caa atc gta acc aac aag gcg act tat gat gtt	962	
78	Glu Gly Tyr Val Ser Gln Ile Val Thr Asn Lys Ala Thr Tyr Asp Val		
79	225 230 235		
80	gat ctt gtc atc aat tgt att ggt ttt act gcc aac agt gcc ttg gca	1010	
81	Asp Leu Val Ile Asn Cys Ile Gly Phe Thr Ala Asn Ser Ala Leu Ala		
82	240 245 250		
83	agt gat aag tta gct acc ttc aaa aat ggc gca atc aag gtg gat aag	1058	
84	Ser Asp Lys Leu Ala Thr Phe Lys Asn Gly Ala Ile Lys Val Asp Lys		
85	255 260 265		
86	cat .caa caa agt agt gat cca gat gtt tac gcg gta ggt gat gtt gcg	1106	
87	His Gln Gln Ser Ser Asp Pro Asp Val Tyr Ala Val Gly Asp Val Ala		
88	270 275 280		
89	aca att tat tct aat gcc ttg caa gat ttt act tat atc gct ctt gcc	1154	
90	Thr Ile Tyr Ser Asn Ala Leu Gln Asp Phe Thr Tyr Ile Ala Leu Ala		
91	285 290 295 300		
92	tca aac gct gtt cggtca gga att gtc gca gga cac aat att ggt gga	1202	
93	Ser Asn Ala Val Arg Ser Gly Ile Val Ala Gly His Asn Ile Gly Gly		

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Input Set : N:\Crf3\RULE60\10718000.raw  
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94	305	310	315	
95	aaa gaa tta gaa tct gtt ggt gtt caa ggt tct aat ggt att tcg att	Lys Glu Leu Glu Ser Val Gly Val Gln Gly Ser Asn Gly Ile Ser Ile		. 1250
96	320	325	330	
97				
98	ttt ggt tac aat atg act tct aca gga ctt tct gtt aaa gct gct aaa	Phe Gly Tyr Asn Met Thr Ser Thr Gly Leu Ser Val Lys Ala Ala Lys		1298
99	Ph			
100	335	340	345	
101	aaa tta ggt tta gaa gtt tca ttt agt gat ttt gaa gat aaa caa aaa	Lys Leu Gly Leu Glu Val Ser Phe Ser Asp Phe Asp Lys Gln Lys		1346
102	350	355	360	
103				
104	gct tgg ttt ctt cat gaa aac aac gat agt gtg aaa att cgt atc gta	Ala Trp Phe Leu His Glu Asn Asn Asp Ser Val Lys Ile Arg Ile Val		1394
105	Ala			
106	365	370	375	380
107	tat gag aca aaa agt cgc aga att att gga gca caa ctt gct agt aaa	Tyr Glu Thr Lys Ser Arg Arg Ile Ile Gly Ala Gln Leu Ala Ser Lys		1442
108	Tyr			
109	385	390	395	
110	agt gag ata att gca gga aat ata aat atg ttc agt tta gcg att caa	Ser Glu Ile Ile Ala Gly Asn Ile Asn Met Phe Ser Leu Ala Ile Gln		1490
111	Ser			
112	400	405	410	
113	gag aaa aaa aca att gat gaa cta gct ttg ctt gat tta ttc ttt ctc	Glu Lys Lys Thr Ile Asp Glu Leu Ala Leu Leu Asp Leu Phe Leu		1538
114	Glu			
115	415	420	425	
116	ccc cac ttc aac agt cca tat aat tat atg aca gtt gca gct	Pro His Phe Asn Ser Pro Tyr Asn Tyr Met Thr Val Ala Ala		1580
117	Pro			
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119	ttgaatgcc aataaacaat agaaaatctat ctgcattgata gatttttta ttttttag			1638
121 <210>	SEQ ID NO: 2			
122 <211>	LENGTH: 442			
123 <212>	TYPE: PRT			
124 <213>	ORGANISM: Lactococcus lactis			
125 <400>	SEQUENCE: 2			
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128	Asn Thr Leu Leu Glu Gln Tyr Pro Gly His Glu Ile Val Met Ile Asp			
129	20	25	30	
130	Arg Asn Ser Asn Met Ser Tyr Leu Gly Cys Gly Thr Ala Ile Trp Val			
131	35	40	45	
132	Gly Arg Gln Ile Glu Lys Pro Asp Glu Leu Phe Tyr Ala Lys Ala Glu			
133	50	55	60	
134	Asp Phe Glu Ala Lys Gly Val Lys Ile Leu Thr Glu Thr Glu Val Ser			
135	65	70	75	80
136	Glu Ile Asp Phe Ala Asn Lys Lys Val Tyr Ala Lys Thr Lys Ser Asp			
137	85	90	95	
138	Asp Glu Ile Ile Glu Ala Tyr Asp Lys Leu Val Leu Ala Thr Gly Ser			
139	100	105	110	
140	Arg Pro Ile Ile Pro Asn Leu Pro Gly Lys Asp Leu Lys Gly Ile His			
141	115	120	125	
142	Phe Leu Lys Leu Phe Gln Glu Gly Gln Ala Ile Asp Ala Glu Phe Ala			
143	130	135	140	

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144 Lys Glu Lys Val Lys Arg Ile Ala Val Ile Gly Ala Gly Tyr Ile Gly
145 145 150 155 160
146 Thr Glu Ile Ala Glu Ala Ala Lys Arg Arg Gly Lys Glu Val Leu Leu
147 165 170 175
148 Phe Asp Ala Glu Asn Thr Ser Leu Ala Ser Tyr Tyr Asp Glu Glu Phe
149 180 185 190
150 Ala Lys Gly Met Asp Glu Asn Leu Ala Gln His Gly Ile Glu Leu His
151 195 200 205
152 Phe Gly Gln Leu Ala Lys Glu Phe Lys Ala Asn Glu Glu Gly Tyr Val
153 210 215 220
154 Ser Gln Ile Val Thr Asn Lys Ala Thr Tyr Asp Val Asp Leu Val Ile
155 225 230 235 240
156 Asn Cys Ile Gly Phe Thr Ala Asn Ser Ala Leu Ala Ser Asp Lys Leu
157 245 250 255
158 Ala Thr Phe Lys Asn Gly Ala Ile Lys Val Asp Lys His Gln Gln Ser
159 260 265 270
160 Ser Asp Pro Asp Val Tyr Ala Val Gly Asp Val Ala Thr Ile Tyr Ser
161 275 280 285
162 Asn Ala Leu Gln Asp Phe Thr Tyr Ile Ala Leu Ala Ser Asn Ala Val
163 290 295 300
164 Arg Ser Gly Ile Val Ala Gly His Asn Ile Gly Gly Lys Glu Leu Glu
165 305 310 315 320
166 Ser Val Gly Val Gln Gly Ser Asn Gly Ile Ser Ile Phe Gly Tyr Asn
167 325 330 335
168 Met Thr Ser Thr Gly Leu Ser Val Lys Ala Ala Lys Lys Leu Gly Leu
169 340 345 350
170 Glu Val Ser Phe Ser Asp Phe Glu Asp Lys Gln Lys Ala Trp Phe Leu
171 355 360 365
172 His Glu Asn Asn Asp Ser Val Lys Ile Arg Ile Val Tyr Glu Thr Lys
173 370 375 380
174 Ser Arg Arg Ile Ile Gly Ala Gln Leu Ala Ser Lys Ser Glu Ile Ile
175 385 390 395 400
176 Ala Gly Asn Ile Asn Met Phe Ser Leu Ala Ile Gln Glu Lys Lys Thr
177 405 410 415
178 Ile Asp Glu Leu Ala Leu Leu Asp Leu Phe Phe Leu Pro His Phe Asn
179 420 425 430
180 Ser Pro Tyr Asn Tyr Met Thr Val Ala Ala
181 435 440

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/718,000

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Input Set : N:\Crf3\RULE60\10718000.raw  
Output Set: N:\CRF4\08272004\J718000.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\10718000.raw

Output Set: N:\CRF4\08272004\J718000.raw

L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0